

## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

(i) APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu Bala; Waterfield, Michael Derek; Parker, Peter Joseph; Otsu, Masayuki; Panayotou, George; Volinia, Stefano; Gout, Ivan Tarasovitch

(ii) TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY, THEIR PREPARATION AND USE

(iii) NUMBER OF SEQUENCES: 50

#### (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Felfe & Lynch  
(B) STREET: 805 Third Avenue  
(C) CITY: New York  
(D) STATE: New York  
(E) COUNTRY: USA  
(F) ZIP: 10022

#### (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
(B) COMPUTER: IBM PS/2  
(C) OPERATING SYSTEM: PC-DOS  
(D) SOFTWARE: Wordperfect

#### (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/162,081  
(B) FILING DATE: February 7, 1994  
(C) CLASSIFICATION: 435

#### (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/GB93/00761  
(B) FILING DATE: 13 April 1993

#### (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Pasqualini, Patricia A.  
(B) REGISTRATION NUMBER: 34,894  
(C) REFERENCE/DOCKET NUMBER: LUD 5256

#### (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 688-9200  
(B) TELEFAX: (212) 838-3884

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 12 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Gly Glu Ser Asp Gly Gly Tyr Met Asp Met Ser Lys  
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Asp Met Ser Lys Asp Glu Ser Val Asp Tyr Val Pro Met Leu Asp Met  
 1 5 10 15  
  
Lys

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Cys Asp Glu Ser Val Asp Tyr Val Pro Met Leu  
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 17 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Ala Arg Asp Ile Met Arg Asp Ser Asn Tyr Ile Ser Lys Gly Ser Thr  
1 5 10 15

Phe

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Glu Phe Cys Pro Asp Pro Leu Tyr Glu Val Met Leu Lys  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Arg Arg Phe Thr Ser Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Arg Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Thr Leu Ala Tyr Pro Val Tyr Ala Gln Gln Arg Arg  
1                   5                   10

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Thr Leu Ala His Pro Val Arg Ala Pro Gly Pro Gly Pro Pro Ala Ala  
1                   5                   10                   15  
Arg

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Tyr Xaa Xaa Met  
1

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Met Asp Trp Ile Phe His Thr  
1 5

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AARATGGAYT GGATHTTYCA YAC

23

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Asp Asp Gly Gln Leu Phe His Ile Asp Phe Gly His Phe  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GATGATGGCC ARCTGTTYCA YATWGAYTTT GGCCA

35

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

AATTCACACA CTGGCATGCC GAT

23

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GACTCGAGTC GACATCGATT TTTTTTTTTT TTTT

35

(2) INFORMATION FOR SEQ ID NO: 17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TTTAAGCTTA GGCATTCTAA AGTCACTATC ATCCC

35

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GACTCGAGTC GACATCGA

18

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

CAGGCCTGGC TTCCTGT

17

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

AACCAGGCTC AACTGTT

17

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TGCTGTAAAT TCTAATGCTG

20

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

GTATTTTCATG AAACAAATGA

20

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Cys	Lys	Met	Asp	Trp	Ile	Phe	His	Thr	Ile	Lys	Gln	His	Ala	Leu	Asn
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

AAGGATCAGA ACAATGCCT

19

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

AGGCTTTCTT TAGCCATCA

19

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Gly	Asp	Asp	Leu	Arg	Gln	Asp
1				5		

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single



(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GGNGAYGAYY TRCGNCARGA

20

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Phe His Ile Asp Phe Gly His Phe  
1 5

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

RAARTGCCRA ARTCDATRTG RAA

23

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 11 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Glu Glu Glu Glu Glu Tyr Met Pro Met Xaa Xaa  
1 5 10

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid

(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Asp Asp Asp Asp Asp Val  
1 5

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3412 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single or double  
(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..3204  
(D) OTHER INFORMATION: /standard\_name= "CDS"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

ATG CCT CCA AGA CCA TCA TCA GGT GAA CTG TGG GGC ATC CAC TTG ATG	48
Met Pro Pro Arg Pro Ser Ser Gly Glu Leu Trp Gly Ile His Leu Met	
1 5 10 15	
CCC CCA AGA ATC CTA GTG GAA TGT TTA CTA CCA AAT GGA ATG ATA GTG	96
Pro Pro Arg Ile Leu Val Glu Cys Leu Leu Pro Asn Gly Met Ile Val	
20 25 30	
ACT TTA GAA TGC CTC CGT GAG GCT ACA TTA GTA ACT ATA AAG CAT GAA	144
Thr Leu Glu Cys Leu Arg Glu Ala Thr Leu Val Thr Ile Lys His Glu	
35 40 45	
CTA TTT AAA GAA GCA AGA AAA TAC CCT CTC CAT CAA CTT CTT CAA GAT	192
Leu Phe Lys Glu Ala Arg Lys Tyr Pro Leu His Gln Leu Leu Gln Asp	
50 55 60	
GAA TCT TCT TAC ATT TTC GTA AGT GTT ACC CAA GAA GCA GAA AGG GAA	240
Glu Ser Ser Tyr Ile Phe Val Ser Val Thr Gln Glu Ala Glu Arg Glu	
65 70 75 80	
GAA TTT TTT GAT GAA ACA AGA CGA CTT TGT GAT CTT CGG CTT TTT CAA	288
Glu Phe Phe Asp Glu Thr Arg Arg Leu Cys Asp Leu Arg Leu Phe Gln	
85 90 95	

CCA	TTT	TTA	AAA	GTA	ATT	GAA	CCA	GTA	GGC	AAC	CGT	GAA	GAA	AAG	ATC	336
Pro	Phe	Leu	Lys	Val	Ile	Glu	Pro	Val	Gly	Asn	Arg	Glu	Glu	Lys	Ile	
			100					105					110			
CTC	AAT	CGA	GAA	ATT	GGT	TTT	GCT	ATC	GGC	ATG	CCA	GTG	TGC	GAA	TTT	384
Leu	Asn	Arg	Glu	Ile	Gly	Phe	Ala	Ile	Gly	Met	Pro	Val	Cys	Glu	Phe	
		115					120					125				
GAT	ATG	GTT	AAA	GAT	CCT	GAA	GTA	CAG	GAC	TTC	CGA	AGA	AAT	ATT	CTT	432
Asp	Met	Val	Lys	Asp	Pro	Glu	Val	Gln	Asp	Phe	Arg	Arg	Asn	Ile	Leu	
	130					135					140					
AAT	GTT	TGT	AAA	GAA	GCT	GTG	GAT	CTT	AGG	GAT	CTT	AAT	TCA	CCT	CAT	480
Asn	Val	Cys	Lys	Glu	Ala	Val	Asp	Leu	Arg	Asp	Leu	Asn	Ser	Pro	His	
145					150					155					160	
AGT	AGA	GCA	ATG	TAT	GTC	TAT	CCG	CCA	CAT	GTA	GAA	TCT	TCA	CCA	GAG	528
Ser	Arg	Ala	Met	Tyr	Val	Tyr	Pro	Pro	His	Val	Glu	Ser	Ser	Pro	Glu	
				165					170					175		
CTG	CCA	AAG	CAC	ATA	TAT	AAT	AAA	TTG	GAT	AGA	GGC	CAA	ATA	ATA	GTG	576
Leu	Pro	Lys	His	Ile	Tyr	Asn	Lys	Leu	Asp	Arg	Gly	Gln	Ile	Ile	Val	
			180					185					190			
GTG	ATT	TGG	GTA	ATA	GTT	TCT	CCA	AAT	AAT	GAC	AAG	CAG	AAG	TAT	ACT	624
Val	Ile	Trp	Val	Ile	Val	Ser	Pro	Asn	Asn	Asp	Lys	Gln	Lys	Tyr	Thr	
		195					200					205				
CTG	AAA	ATC	AAC	CAT	GAC	TGT	GTG	CCA	GAA	CAA	GTA	ATT	GCT	GAA	GCA	672
Leu	Lys	Ile	Asn	His	Asp	Cys	Val	Pro	Glu	Gln	Val	Ile	Ala	Glu	Ala	
	210					215					220					
ATC	AGG	AAA	AAA	ACT	AGA	AGT	ATG	TTG	CTA	TCA	TCT	GAA	CAA	TTA	AAA	720
Ile	Arg	Lys	Lys	Thr	Arg	Ser	Met	Leu	Leu	Ser	Ser	Glu	Gln	Leu	Lys	
225					230					235					240	
CTC	TGT	GTT	TTA	GAA	TAT	CAG	GGC	AAG	TAC	ATT	TTA	AAA	GTG	TGT	GGA	768
Leu	Cys	Val	Leu	Glu	Tyr	Gln	Gly	Lys	Tyr	Ile	Leu	Lys	Val	Cys	Gly	
				245				250						255		
TGT	GAT	GAA	TAC	TTC	CTA	GAA	AAA	TAT	CCT	CTG	AGT	CAG	TAT	AAG	TAT	816
Cys	Asp	Glu	Tyr	Phe	Leu	Glu	Lys	Tyr	Pro	Leu	Ser	Gln	Tyr	Lys	Tyr	
			260					265					270			

ATA	AGA	AGC	TGT	ATA	ATG	CTT	GGG	AGG	ATG	CCC	AAT	TTG	AAG	ATG	ATG	864
Ile	Arg	Ser	Cys	Ile	Met	Leu	Gly	Arg	Met	Pro	Asn	Leu	Lys	Met	Met	
		275					280					285				
GCT	AAA	GAA	AGC	CTT	TAT	TCT	CAA	CTG	CCA	ATG	GAC	TGT	TTT	ACA	ATG	912
Ala	Lys	Glu	Ser	Leu	Tyr	Ser	Gln	Leu	Pro	Met	Asp	Cys	Phe	Thr	Met	
	290					295					300					
CCA	TCT	TAT	TCC	AGA	CGC	ATT	TCC	ACA	GCT	ACA	CCA	TAT	ATG	AAT	GGA	960
Pro	Ser	Tyr	Ser	Arg	Arg	Ile	Ser	Thr	Ala	Thr	Pro	Tyr	Met	Asn	Gly	
305					310					315					320	
GAA	ACA	TCT	ACA	AAA	TCC	CTT	TGG	GTT	ATA	AAT	AGA	GCA	CTC	AGA	ATA	1008
Glu	Thr	Ser	Thr	Lys	Ser	Leu	Trp	Val	Ile	Asn	Arg	Ala	Leu	Arg	Ile	
				325					330					335		
AAA	ATT	CTT	TGT	GCA	ACC	TAC	GTG	AAT	CTA	AAT	ATT	CGA	GAC	ATT	GAC	1056
Lys	Ile	Leu	Cys	Ala	Thr	Tyr	Val	Asn	Leu	Asn	Ile	Arg	Asp	Ile	Asp	
			340					345					350			
AAG	ATT	TAT	GTT	CGA	ACA	GGT	ATC	TAC	CAT	GGA	GGA	GAA	CCC	TTA	TGT	1104
Lys	Ile	Tyr	Val	Arg	Thr	Gly	Ile	Tyr	His	Gly	Gly	Glu	Pro	Leu	Cys	
		355					360					365				
GAC	AAT	GTG	AAC	ACT	CAA	AGA	GTA	CCT	TGT	TCC	AAT	CCC	AGG	TGG	AAT	1152
Asp	Asn	Val	Asn	Thr	Gln	Arg	Val	Pro	Cys	Ser	Asn	Pro	Arg	Trp	Asn	
	370					375					380					
GAA	TGG	CTG	AAT	TAT	GAT	ATA	TAC	ATT	CCT	GAT	CTT	CCT	CGT	GCT	GCT	1200
Glu	Trp	Leu	Asn	Tyr	Asp	Ile	Tyr	Ile	Pro	Asp	Leu	Pro	Arg	Ala	Ala	
385					390					395					400	
CGA	CTT	TGC	CTT	TCC	ATT	TGC	TCT	GTT	AAA	GGC	CGA	AAG	GGT	GCT	AAA	1248
Arg	Leu	Cys	Leu	Ser	Ile	Cys	Ser	Val	Lys	Gly	Arg	Lys	Gly	Ala	Lys	
				405					410					415		
GAG	GAA	CAC	TGT	CCA	TTG	GCA	TGG	GGA	AAT	ATA	AAC	TTG	TTT	GAT	TAC	1296
Glu	Glu	His	Cys	Pro	Leu	Ala	Trp	Gly	Asn	Ile	Asn	Leu	Phe	Asp	Tyr	
			420					425					430			
ACA	GAC	ACT	CTA	GTA	TCT	GGA	AAA	ATG	GCT	TTG	AAT	CTT	TGG	CCA	GTA	1344
Thr	Asp	Thr	Leu	Val	Ser	Gly	Lys	Met	Ala	Leu	Asn	Leu	Trp	Pro	Val	
		435					440					445				
CCT	CAT	GGA	TTA	GAA	GAT	TTG	CTG	AAC	CCT	ATT	GGT	GTT	ACT	GGA	TCA	1392

Pro	His	Gly	Leu	Glu	Asp	Leu	Leu	Asn	Pro	Ile	Gly	Val	Thr	Gly	Ser
450						455					460				

AAT	CCA	AAT	AAA	GAA	ACT	CCA	TGC	TTA	GAG	TTG	GAG	TTT	GAC	TGG	TTC	1440
Asn	Pro	Asn	Lys	Glu	Thr	Pro	Cys	Leu	Glu	Leu	Glu	Phe	Asp	Trp	Phe	
465					470				475						480	

AGC	AGT	GTG	GTA	AAG	TTC	CCA	GAT	ATG	TCA	GTG	ATT	GAA	GAG	CAT	GCC	1488
Ser	Ser	Val	Val	Lys	Phe	Pro	Asp	Met	Ser	Val	Ile	Glu	Glu	His	Ala	
				485					490					495		

AAT	TGG	TCT	GTA	TCC	CGA	GAA	GCA	GGA	TTT	AGC	TAT	TCC	CAC	GCA	GGA	1536
Asn	Trp	Ser	Val	Ser	Arg	Glu	Ala	Gly	Phe	Ser	Tyr	Ser	His	Ala	Gly	
			500					505					510			

CTG	AGT	AAC	AGA	CTA	GCT	AGA	GAC	AAT	GAA	TTA	AGG	GAA	AAT	GAC	AAA	1584
Leu	Ser	Asn	Arg	Leu	Ala	Arg	Asp	Asn	Glu	Leu	Arg	Glu	Asn	Asp	Lys	
		515					520					525				

GAA	CAG	CTC	AAA	GCA	ATT	TCT	ACA	CGA	GAT	CCT	CTC	TCT	GAA	ATC	ACT	1632
Glu	Gln	Leu	Lys	Ala	Ile	Ser	Thr	Arg	Asp	Pro	Leu	Ser	Glu	Ile	Thr	
	530					535					540					

GAG	CAG	GAG	AAA	GAT	TTT	CTA	TGG	AGT	CAC	AGA	CAC	TAT	TGT	GTA	ACT	1680
Glu	Gln	Glu	Lys	Asp	Phe	Leu	Trp	Ser	His	Arg	His	Tyr	Cys	Val	Thr	
545				550					555						560	

ATC	CCC	GAA	ATT	CTA	CCC	AAA	TTG	CTT	CTG	TCT	GTT	AAA	TGG	AAT	TCT	1728
Ile	Pro	Glu	Ile	Leu	Pro	Lys	Leu	Leu	Leu	Ser	Val	Lys	Trp	Asn	Ser	
				565					570					575		

AGA	GAT	GAA	GTA	GCC	CAG	ATG	TAT	TGC	TTG	GTA	AAA	GAT	TGG	CCT	CCA	1776
Arg	Asp	Glu	Val	Ala	Gln	Met	Tyr	Cys	Leu	Val	Lys	Asp	Trp	Pro	Pro	
			580					585					590			

ATC	AAA	CCT	GAA	CAG	GCT	ATG	GAA	CTT	CTG	GAC	TGT	AAT	TAC	CCA	GAT	1824
Ile	Lys	Pro	Glu	Gln	Ala	Met	Glu	Leu	Leu	Asp	Cys	Asn	Tyr	Pro	Asp	
		595					600					605				

CCT	ATG	GTT	CGA	GGT	TTT	GCT	GTT	CGG	TGC	TTG	GAA	AAA	TAT	TTA	ACA	1872
Pro	Met	Val	Arg	Gly	Phe	Ala	Val	Arg	Cys	Leu	Glu	Lys	Tyr	Leu	Thr	
	610					615					620					

GAT Asp 625	GAC Asp	AAA Lys	CTT Leu	TCT Ser	CAG Gln 630	TAT Tyr	TTA Leu	ATT Ile	CAG Gln	CTA Leu 635	GTA Val	CAG Gln	GTC Val	CTA Leu	AAA Lys 640	1920
TAT Tyr	GAA Glu	CAA Gln	TAT Tyr	TTG Leu 645	GAT Asp	AAC Asn	TTG Leu	CTT Leu	GTG Val 650	AGA Arg	TTT Phe	TTA Leu	CTG Leu	AAG Lys 655	AAA Lys	1968
GCA Ala	TTG Leu	ACT Thr	AAT Asn 660	CAA Gln	AGG Arg	ATT Ile	GGG Gly	CAC His 665	TTT Phe	TTC Phe	TTT Phe	TGG Trp	CAT His 670	TTA Leu	AAA Lys	2016
TCT Ser	GAG Glu	ATG Met 675	CAC His	AAT Asn	AAA Lys	ACA Thr	GTT Val 680	AGC Ser	CAG Gln	AGG Arg	TTT Phe	GGC Gly 685	CTG Leu	CTT Leu	TTG Leu	2064
GAG Glu 690	TCC Ser	TAT Tyr	TGT Cys	CGT Arg	GCA Ala	TGT Cys 695	GGG Gly	ATG Met	TAT Tyr	TTG Leu	AAG Lys 700	CAC His	CTG Leu	AAT Asn	AGG Arg	2112
CAA Gln 705	GTC Val	GAG Glu	GCA Ala	ATG Met	GAA Glu 710	AAG Lys	CTC Leu	ATT Ile	AAC Asn	TTA Leu 715	ACT Thr	GAC Asp	ATT Ile	CTC Leu	AAA Lys 720	2160
CAG Gln	GAG Glu	AGG Arg	AAG Lys	GAT Asp 725	GAA Glu	ACA Thr	CAA Gln	AAG Lys	GTA Val 730	CAG Gln	ATG Met	AAG Lys	TTT Phe	TTA Leu 735	GTT Val	2208
GAG Glu	CAA Gln	ATG Met	AGG Arg	CGA Arg	CCA Pro	GAT Asp	TTC Phe	ATG Met	GAT Asp	GCC Ala	CTA Leu	CAG Gln	GGC Gly 750	TTG Leu	CTG Leu	2256
TCT Ser	CCT Pro	CTA Leu 755	AAC Asn	CCT Pro	GCT Ala	CAT His	CAA Gln 760	CTA Leu	GGA Gly	AAC Asn	CTC Leu	AGG Arg 765	CTT Leu	AAA Lys	GAG Glu	2304
TGT Cys 770	CGA Arg	ATT Ile	ATG Met	TCT Ser	TCT Ser	GCA Ala 775	AAA Lys	AGG Arg	CCA Pro	CTG Leu	TGG Trp 780	TTG Leu	AAT Asn	TGG Trp	GAG Glu	2352
AAC Asn 785	CCA Pro	GAC Asp	ATC Ile	ATG Met	TCA Ser 790	GAG Glu	TTA Leu	CTG Leu	TTT Phe	CAG Gln 795	AAC Asn	AAT Asn	GAG Glu	ATC Ile	ATC Ile 800	2400

TTT	AAA	AAT	GGG	GAT	GAT	TTA	CGG	CAA	GAT	ATG	CTA	ACA	CTT	CAA	ATT	2448
Phe	Lys	Asn	Gly	Asp	Asp	Leu	Arg	Gln	Asp	Met	Leu	Thr	Leu	Gln	Ile	
			805						810					815		
ATT	CGT	ATT	ATG	GAA	AAT	ATC	TGG	CAA	AAT	CAA	GGT	CTT	GAT	CTT	CGA	2496
Ile	Arg	Ile	Met	Glu	Asn	Ile	Trp	Gln	Asn	Gln	Gly	Leu	Asp	Leu	Arg	
			820					825					830			
ATG	TTA	CCT	TAT	GGT	TGT	CTG	TCA	ATC	GGT	GAC	TGT	GTG	GGA	CTT	ATT	2544
Met	Leu	Pro	Tyr	Gly	Cys	Leu	Ser	Ile	Gly	Asp	Cys	Val	Gly	Leu	Ile	
		835					840					845				
GAG	GTG	GTG	CGA	AAT	TCT	CAC	ACT	ATT	ATG	CAA	ATT	CAG	TGC	AAA	GGC	2592
Glu	Val	Val	Arg	Asn	Ser	His	Thr	Ile	Met	Gln	Ile	Gln	Cys	Lys	Gly	
	850					855					860					
GGC	TTG	AAA	GGT	GCA	CTG	CAG	TTC	AAC	AGC	CAC	ACA	CTA	CAT	CAG	TGG	2640
Gly	Leu	Lys	Gly	Ala	Leu	Gln	Phe	Asn	Ser	His	Thr	Leu	His	Gln	Trp	
865					870					875					880	
CTC	AAA	GAC	AAG	AAC	AAA	GGA	GAA	ATA	TAT	GAT	GCA	GCC	ATT	GAC	CTG	2688
Leu	Lys	Asp	Lys	Asn	Lys	Gly	Glu	Ile	Tyr	Asp	Ala	Ala	Ile	Asp	Leu	
				885					890					895		
TTT	ACA	CGT	TCA	TGT	GCT	GGA	TAC	TGT	GTA	GCT	ACC	TTC	ATT	TTG	GGA	2736
Phe	Thr	Arg	Ser	Cys	Ala	Gly	Tyr	Cys	Val	Ala	Thr	Phe	Ile	Leu	Gly	
			900					905					910			
ATT	GGA	GAT	CGT	CAC	AAT	AGT	AAC	ATC	ATG	GTG	AAA	GAC	GAT	GGA	CAA	2784
Ile	Gly	Asp	Arg	His	Asn	Ser	Asn	Ile	Met	Val	Lys	Asp	Asp	Gly	Gln	
		915					920					925				
CTG	TTT	CAT	ATA	GAT	TTT	GGA	CAC	TTT	TTG	GAT	CAC	AAG	AAG	AAA	AAA	2832
Leu	Phe	His	Ile	Asp	Phe	Gly	His	Phe	Leu	Asp	His	Lys	Lys	Lys	Lys	
	930					935					940					
TTT	GGT	TAT	AAA	CGA	GAA	CGT	GTG	CCA	TTT	GTT	TTG	ACA	CAG	GAT	TTC	2880
Phe	Gly	Tyr	Lys	Arg	Glu	Arg	Val	Pro	Phe	Val	Leu	Thr	Gln	Asp	Phe	
945					950					955					960	
TTA	ATA	GTG	ATT	AGT	AAA	GGA	GCC	CAA	GAA	TGC	ACA	AAG	ACA	AGA	GAA	2928
Leu	Ile	Val	Ile	Ser	Lys	Gly	Ala	Gln	Glu	Cys	Thr	Lys	Thr	Arg	Glu	
				965					970					975		

TTT	GAG	AGG	TTT	CAG	GAG	ATG	TGT	TAC	AAG	GCT	TAT	CTA	GCT	ATT	CGA	2976
Phe	Glu	Arg	Phe	Gln	Glu	Met	Cys	Tyr	Lys	Ala	Tyr	Leu	Ala	Ile	Arg	
			980					985					990			

CAG	CAT	GCC	AAT	CTC	TTC	ATA	AAT	CTT	TTC	TCA	ATG	ATG	CTT	GGC	TCT	3024
Gln	His	Ala	Asn	Leu	Phe	Ile	Asn	Leu	Phe	Ser	Met	Met	Leu	Gly	Ser	
		995					1000					1005				

GGA	ATG	CCA	GAA	CTA	CAA	TCT	TTT	GAT	GAC	ATT	GCA	TAC	ATT	CGA	AAG	3072
Gly	Met	Pro	Glu	Leu	Gln	Ser	Phe	Asp	Asp	Ile	Ala	Tyr	Ile	Arg	Lys	
	1010					1015					1020					

ACC	CTA	GCC	TTA	GAT	AAA	ACT	GAG	CAA	GAG	GCT	TTG	GAG	TAT	TTC	ATG	3120
Thr	Leu	Ala	Leu	Asp	Lys	Thr	Glu	Gln	Glu	Ala	Leu	Glu	Tyr	Phe	Met	
	1025				1030					1035					1040	

AAA	CAA	ATG	AAT	GAT	GCA	CAT	CAT	GGT	GGC	TGG	ACA	ACA	AAA	ATG	GAT	3168
Lys	Gln	Met	Asn	Asp	Ala	His	His	Gly	Gly	Trp	Thr	Thr	Lys	Met	Asp	
			1045					1050						1055		

TGG	ATC	TTC	CAC	ACA	ATT	AAA	CAG	CAT	GCA	TTG	AAC	TGAAAGATAA				3214
Trp	Ile	Phe	His	Thr	Ile	Lys	Gln	His	Ala	Leu	Asn					
			1060					1065								

CTGAGAAAAT	GAAAGCTCAC	TCTGGACACT	ACACTGCACT	GTTAATAACT	CTCAGCAGGC											3274
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AAAGACCGAT	TGCATAGGAA	TTGCACAATC	CATGAACAGC	ATTAGATTTA	CAGCAAGAAC											3334
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AGAAATAAAA	TACTATATAA	TTTAAATAAT	GTAAACGCAA	ACAGGGTTTG	ATAGCACTTA											3394
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AACTAGTTCA	TTTCAAAA															3412
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(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 868 amino acids residues
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Asn	Ile	Thr	Phe	Cys	Val	Ser	Gln	Asp	Leu	Asp	Val	Pro	Leu	Lys	Val
1				5					10					15	

Lys	Ile	Lys	Ser	Leu	Glu	Gly	His	Lys	Pro	Leu	Leu	Lys	Pro	Ser	Gln
			20					25					30		

Lys	Ile	Leu	Asn	Pro	Glu	Leu	Met	Leu	Ile	Gly	Ser	Asn	Val	Phe	Pro
		35					40					45			



Ser Ser Asp Leu Ile Val Ser Leu Gln Val Phe Asp Lys Glu Arg Asn  
50 55 60

Arg Asn Leu Thr Leu Pro Ile Tyr Thr Pro Tyr Ile Pro Phe Arg Asn  
65 70 75 80

Ser Arg Thr Trp Asp Tyr Trp Leu Thr Leu Pro Ile Arg Ile Lys Gln  
85 90 95

Leu Thr Phe Ser Ser His Leu Arg Ile Ile Leu Trp Glu Tyr Asn Gly  
100 105 110

Ser Lys Gln Ile Pro Phe Phe Asn Leu Glu Thr Ser Ile Phe Asn Leu  
115 120 125

Lys Asp Cys Thr Leu Lys Arg Gly Phe Glu Ser Leu Lys Phe Arg Tyr  
130 135 140

Asp Val Ile Asp His Cys Glu Val Val Thr Asp Asn Lys Asp Gln Glu  
145 150 155 160

Asn Leu Asn Lys Tyr Phe Gln Gly Glu Phe Thr Arg Leu Pro Trp Leu  
165 170 175

Asp Glu Ile Thr Ile Ser Lys Leu Arg Lys Gln Arg Glu Asn Arg Thr  
180 185 190

Trp Pro Gln Gly Thr Phe Val Leu Asn Leu Glu Phe Pro Met Leu Glu  
195 200 205

Leu Pro Val Val Phe Ile Glu Arg Glu Ile Met Asn Thr Gln Met Asn  
210 215 220

Ile Pro Thr Leu Lys Asn Asn Pro Gly Leu Ser Thr Asp Leu Arg Glu  
225 230 235 240

Pro Asn Arg Asn Asp Pro Gln Ile Lys Ile Ser Leu Gly Asp Lys Tyr  
245 250 255

His Ser Thr Leu Lys Phe Tyr Asp Pro Asp Gln Pro Asn Asn Asp Pro  
260 265 270

Ile Glu Glu Lys Tyr Arg Arg Leu Glu Arg Ala Ser Lys Asn Ala Asn  
275 280 285

Leu Asp Lys Gln Val Lys Pro Asp Ile Lys Lys Arg Asp Tyr Leu Asn  
290 295 300

Lys Ile Ile Asn Tyr Pro Pro Gly Thr Lys Leu Thr Ala His Glu Lys  
305 310 315 320

Gly Ser Ile Trp Lys Tyr Arg Tyr Tyr Leu Met Asn Asn Lys Lys Ala  
325 330 335

Leu Thr Lys Leu Leu Gln Ser Thr Asn Leu Arg Glu Glu Ser Glu Arg  
340 345 350

Val Glu Val Leu Glu Leu Met Asp Ser Trp Ala Glu Ile Asp Ile Asp  
355 360 365

Asp Ala Leu Glu Leu Leu Gly Ser Thr Phe Lys Asn Leu Ser Val Arg  
370 375 380

Ser Tyr Ala Val Asn Arg Leu Lys Lys Ala Ser Asp Lys Glu Leu Glu  
385 390 395 400

Leu Tyr Leu Leu Gln Leu Val Glu Ala Val Cys Phe Glu Asn Leu Ser  
405 410 415

Thr Phe Ser Asp Lys Ser Asn Ser Glu Phe Thr Ile Val Asp Ala Val  
420 425 430

Ser Ser Gln Lys Leu Ser Gly Asp Ser Met Leu Leu Ser Thr Ser His  
435 440 445

Ala Asn Gln Lys Leu Leu Lys Ser Ile Ser Ser Glu Ser Glu Thr Ser  
450 455 460

Gly Thr Glu Ser Leu Pro Ile Val Ile Ser Pro Leu Ala Glu Phe Leu  
465 470 475 480

Ile Arg Arg Ala Leu Val Asn Pro Arg Leu Gly Ser Phe Phe Tyr Trp  
485 490 495

Tyr Leu Lys Ser Glu Ser Glu Asp Lys Pro Tyr Leu Asp Gln Ile Leu  
500 505 510

Ser Ser Phe Trp Ser Arg Leu Asp Lys Lys Ser Arg Asn Ile Leu Asn  
515 520 525

Asp Gln Val Arg Leu Ile Asn Val Leu Arg Glu Cys Cys Glu Thr Ile  
530 535 540

Lys Arg Leu Lys Asp Thr Thr Ala Lys Lys Met Glu Leu Leu Val His  
545 550 555 560

Leu Leu Glu Thr Lys Val Arg Pro Leu Val Lys Val Arg Pro Ile Ala  
565 570 575

Leu Pro Leu Asp Pro Asp Val Leu Ile Cys Asp Val Cys Pro Glu Thr  
580 585 590

Ser Lys Val Phe Lys Ser Ser Leu Ser Pro Leu Lys Ile Thr Phe Lys  
595 600 605

Thr Thr Leu Asn Gln Pro Tyr His Leu Met Phe Lys Val Gly Asp Asp  
610 615 620

Leu Arg Gln Asp Gln Leu Val Val Gln Ile Ile Ser Leu Met Asn Glu  
625 630 635 640

Leu Leu Lys Asn Glu Asn Val Asp Leu Lys Leu Thr Pro Tyr Lys Ile  
645 650 655

Leu Ala Thr Gly Pro Gln Glu Gly Ala Ile Glu Phe Ile Pro Asn Asp  
660 665 670

Thr Leu Ala Ser Ile Leu Ser Lys Tyr His Gly Ile Leu Gly Tyr Leu  
675 680 685

Lys Leu His Tyr Pro Asp Glu Asn Ala Thr Leu Gly Val Gln Gly Trp  
690 695 700

Val Leu Asp Asn Phe Val Lys Ser Cys Ala Gly Tyr Cys Val Ile Thr  
705 710 715 720

Tyr Ile Leu Gly Val Gly Asp Arg His Leu Asp Asn Leu Leu Val Thr  
725 730 735

Pro Asp Gly His Phe Phe His Ala Asp Phe Gly Tyr Ile Leu Gly Gln  
740 745 750

Asp Pro Lys Pro Phe Pro Pro Leu Met Lys Leu Pro Pro Gln Ile Ile  
755 760 765

Glu Ala Phe Gly Gly Ala Glu Ser Ser Asn Tyr Asp Lys Phe Arg Ser  
770 775 780

Tyr Cys Phe Val Ala Tyr Ser Ile Leu Arg Arg Asn Ala Gly Leu Ile  
785 790 795 800

Leu Asn Leu Phe Glu Leu Met Lys Thr Ser Asn Ile Pro Asp Ile Arg  
805 810 815

Ile Asp Pro Asn Gly Ala Ile Leu Arg Val Arg Glu Arg Phe Asn Leu  
820 825 830

Asn Met Ser Glu Glu Asp Ala Thr Val His Phe Gln Asn Leu Ile Asn  
835 840 845

Asp Ser Val Asn Ala Leu Leu Pro Ile Val Ile Asp His Leu His Asn  
850 855 860

Leu Ala Gln Tyr  
865

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3240 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

ATGCCTCCAA GACCATCATC AGGTGAACTG TGGGGCATCC ACTTGATGCC CCCAAGAATC	60
CTAGTGGAAT GTTTACTACC AAATGGAATG ATAGTGACTT TAGAATGCCT CCGTGAGGCT	120
ACATTAGTAA CTATAAAGCA TGA ACTATTT AAAGAAGCAA GAAAATACCC TCTCCATCAA	180
CTTCTTCAAG ATGAATCTTC TTACATTTTC GTAAGTGTTA CCCAAGAAGC AGAAAGGGAA	240
GAATTTTTTG ATGAAACAAG ACGACTTTGT GATCTTCGGC TTTTCAACC ATTTTAAAA	300
GTAATTGAAC CAGTAGGCAA CCGTGAAGAA AAGATCCTCA ATCGAGAAAT TGGTTTTGCT	360

ATCGGCATGC CAGTGTGCGA ATTTGATATG GTTAAAGATC CTGAAGTACA GGACTTCCGA	420
AGAAATATTC TTAATGTTTG TAAAGAAGCT GTGGATCTTA GGGATCTTAA TTCACCTCAT	480
AGTAGAGCAA TGTATGTCTA TCCGCCACAT GTAGAATCTT CACCAGAGCT GCCAAAGCAC	540
ATATATAATA AATTGGATAG AGGCCAAATA ATAGTGGTGA TTTGGGTAAT AGTTTCTCCA	600
AATAATGACA AGCAGAAGTA TACTCTGAAA ATCAACCATG ACTGTGTGCC AGAACAAGTA	660
ATTGCTGAAG CAATCAGGAA AAAAAGTAGA AGTATGTTGC TATCATCTGA ACAATTAAAA	720
CTCTGTGTTT TAGAATATCA GGGCAAGTAC ATTTTAAAAG TGTGTGGATG TGATGAATAC	780
TTCCTAGAAA AATATCCTCT GAGTCAGTAT AAGTATATAA GAAGCTGTAT AATGCTTGGG	840
AGGATGCCCCA ATTTGAAGAT GATGGCTAAA GAAAGCCTTT ATTCTCAACT GCCAATGGAC	900
TGTTTTACAA TGCCATCTTA TTCCAGACGC ATTTCCACAG CTACACCATA TATGAATGGA	960
GAAACATCTA CAAATCCCT TTGGGTATA AATAGAGCAC TCAGAATAAA AATTCTTTGT	1020
GCAACCTATG TGAATGTAAA TATTCGAGAC ATTGACAAGA TTTATGTTTCG AACAGGTATC	1080
TACCATGGAG GAGAACCCTT ATGTGACAAT GTGAACACTC AAAGAGTACC TTGTTCCAAT	1140
CCCAGGTGGA ATGAATGGCT GAATTATGAT ATATACATTC CTGATCTTCC TCGTGCTGCT	1200
CGACTTTGCC TTTCCAATTG CTCTGTATAA GGCCGAAAGG GTGCTAAAGA GGAACACTGT	1260
CCATTGGCAT GGGGAAATAT AACTTGTTT GATTACACAG ACACTCTAGT ATCTGGAAAA	1320
ATGGCTTTGA ATCTTTGGCC AGTACCTCAT GGATTAGAAG ATTTGCTGAA CCCTATTGGT	1380
GTTACTGGAT CAAATCCAAA TAAAGAACT CCATGCTTAG AGTTGGAGTT TGACTGGTTC	1440
AGCAGTGTGG TAAAGTTCCC AGATATGTCA GTGATTGAAG AGCATGCCAA TTGGTCTGTA	1500
TCCCGAGAAG CAGGATTTAG CTATTCCCAC GCAGGACTGA GTAACAGACT AGCTAGAGAC	1560
AATGAATTAA GGGAAAATGA CAAAGAACAG CTCAAAGCAA TTTCTACACG AGATCCTCTC	1620
TCTGAAATCA CTGAGCAGGA GAAAGATTTT CTATGGAGTC ACAGACACTA TTGTGTAAC	1680
ATCCCCGAAA TTCTACCCAA ATTGCTTCTG TCTGTAAAT GGAATTCTAG AGATGAAGTA	1740
GCCCAGATGT ATTGCTTGGT AAAAGATTGG CCTCCAATCA AACCTGAACA GGCTATGGAA	1800
CTTCTGGACT GTAATTACCC AGATCCTATG GTTCGAGGTT TTGCTGTTCG GTGCTTGGAA	1860
AAATATTTAA CAGATGACAA ACTTTCTCAG TATTTAATTC AGCTAGTACA GGTCCTAAAA	1920
TATGAACAAT ATTTGGATAA CTTGCTTGTG AGATTTTTAC TGAAGAAAGC ATTGACTAAT	1980
CAAAGGATTG GGCACCTTTT CTTTGGCAT TTAAAATCTG AGATGCACAA TAAAACAGTT	2040

AGCCAGAGGT TTGGCCTGCT TTTGGAGTCC TATTGTCGTG CATGTGGGAT GTATTTGAAG	2100
CACCTGAATA GGCAAGTCGA GGCAATGGAA AAGCTCATTA ACTTAACTGA CATTCTCAAA	2160
CAGGAGAGGA AGGATGAAAC ACAAAGGTA CAGATGAAGT TTTTAGTTGA GCAAATGAGG	2220
CGACCAGATT TCATGGATGC CCTACAGGGC TTGCTGTCTC CTCTAAACCC TGCTCATCAA	2280
CTAGGAAACC TCAGGCTTAA AGAGTGTCGA ATTATGTCTT CTGCAAAAAG GCCACTGTGG	2340
TTGAATTGGG AGAACCCAGA CATCATGTCA GAGTTACTGT TTCAGAACAA TGAGATCATC	2400
TTTAAAAATG GGGATGATTT ACGGCAAGAT ATGCTAACAC TTCAAATTAT TCGTATTATG	2460
GAAAATATCT GGCAAAATCA AGGTCTTGAT CTTGGAATGT TACCTTATGG TTGTCTGTCA	2520
ATCGGTGACT GTGTGGGACT TATTGAGGTG GTGCGAAATT CTCACACTAT TATGCAAATT	2580
CAGTGCAAAG GCGGCTTGAA AGGTGCACTG CAGTTCAACA GCCACACACT ACATCAGTGG	2640
CTCAAAGACA AGAACAAAGG AGAAATATAT GATGCAGCCA TTGACCTGTT TACACGTTCA	2700
TGTGCTGGAT ACTGTGTAGC TACCTTCATT TTGGGAATTG GAGATCGTCA CAATAGTAAC	2760
ATCATGGTGA AAGACGATGG ACAACTGTTT CATATAGATT TTGGACACTT TTTGGATCAC	2820
AAGAAGAAAA AATTTGTTA TAAACGAGAA CGTGTGCCAT TTGTTTTGAC ACAGGATTTC	2880
TTAATAGTGA TTAGTAAGG AGCCCAAGAA TGCACAAAGA CAAGAGAATT TGAGAGGTTT	2940
CAGGAGATGT GTTACAAGGC TTATCTAGCT ATTCGACAGC ATGCCAATCT CTTCATAAAT	3000
CTTTTCTCAA TGATGCTTGG CTCTGGAATG CCAGAACTAC AATCTTTTGA TGACATTGCA	3060
TACATTCGAA AGACCCTAGC CTTAGATAAA ACTGAGCAAG AGGCTTTGGA GTATTTTCATG	3120
AAACAAATGA ATGATGCACA TCATGGTGGC TGGACAACAA AAATGGATTG GATCTTCCAC	3180
ACAATTAAAC AGCATGCATT GAACTGAAAG ATAAGTGAAGA AAATGAAAGC TCACTCTGGA	3240

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ATGCCTCCAA GACCATCATC AGGTGAACTG TGGGGCATCC ACTTGATGCC CCCAAGAATC	60
CTAGTAGAAT GTTTACTACC AAATGGGATG ATAGTGACTT TAGAATGCCT CCGTGAGGCT	120

ACGTTAATAA CGATAAAGCA TGAAC TATTT AAAGAAGCAA GAAAATACCC TCTCCATCAA	180
CTTCTTCAAG ATGAATCTTC TTACATTTTC GTAAGTGTTA CCAAGAAGC AGAAAGGGAA	240
GAATTTTTTG ATGAAACAAG ACGACTTGT GACCTTCGGC TTTTCAACC CTTTTTAAAA	300
GTAATTGAAC CAGTAGGCAA CCGTGAAGAA AAGATCCTCA ATCGAGAAAT TGGTTTTGCT	360
ATCGGCATGC CAGTGTGTGA ATTCGATATG GTTAAAGATC CAGAAGTACA GGACTTCCGA	420
AGAAATATTC TCAATGTTTG TAAAGAAGCT GTGGATCTTA GGGATCTTAA TTCACCTCAT	480
AGTAGAGCAA TGTATGTTTA TCCTCCAAAT GTAGAATCTT CACCAGAACT GCCAAAGCAC	540
ATATATAATA AATTGGATAA AGGGCAAATA ATAGTGGTGA TTTGGGTAAT AGTTTCTCCA	600
AATAATGACA AACAGAAGTA TACTCTGAAA ATCAACCATG ACTGTGTGCC AGAACAAGTA	660
ATTGCTGAAG CAATCAGGAA AAAA ACTCGA AGTATGTTGC TATCATCTGA ACAACTAAAA	720
CTCTGTGTTT TAGAATATCA GGGCAAGTAT ATTTTAAAAG TGTGTGGATG TGATGAATAC	780
TTCTTAGAAA AATATCCTCT GAGTCAGTAT AAGTATATAA GAAGCTGTAT AATGCTTGGG	840
AGGATGCCCA ATTTGATGCT GATGGCTAAA GAAAGCCTCT ATTCTCAACT GCCAATGGAC	900
TGTTTTACAA TGCCATCATA TTCCAGACGC ATCTCCACAG CTACGCCATA TATGAATGGA	960
GAAACATCTA CAAAATCCCT TTGGGTATA AATAGTGCAC TCAGAATAAA AATTCTTTGT	1020
GCAACCTATG TGAATGTAAA TATTCGAGAC ATTGACAAGA TTTATGTTTC AACAGGTATC	1080
TACCATGGAG GAGAACCCTT ATGTGATAAT GTGAACACTC AAAGAGTACC TTGTTCCAAT	1140
CCCAGGTGGA ATGAATGGCT GAATTACGAT ATATACATTC CTGATCTTCC TCGTGCTGCT	1200
CGACTTTGCC TTTCCATTG TTCTGTAAA GGCCGAAAGG GTGCTAAAGA GGAACACTGT	1260
CCATTGCCT GGGGAAATAT AACTTGTTT GATTACACAG ATACTCTAGT ATCTGGAAAA	1320
ATGGCTTTGA ATCTTTGGCC AGTACCTCAT GGACTAGAAG ATTTGCTGAA CCCTATTGGT	1380
GTTACTGGAT CAAATCCAAA TAAAGAACT CCATGTTTAG AGTTGGAGTT TGA CTGGTTC	1440
AGCAGTGTGG TAAAGTTTCC AGATATGTCA GTGATTGAAG AGCATGCCAA TTGGTCTGTA	1500
TCCCGTGAAG CAGGATTTAG TTATTCCCAT GCAGGACTGA GTAACAGACT AGCTAGAGAC	1560
AATGAATTAA GAGAAAATGA TAAAGAACAG CTCCGAGCAA TTTGTACACG AGATCCTCTA	1620
TCTGAAATCA CTGAGCAAGA GAAAGATTTT CTGTGGAGCC ACAGACACTA TTGTGTA ACT	1680
ATCCCCGAAA TTCTACCCAA ATTGCTTCTG TCTGTAAAT GGA ACTCTAG AGATGAAGTA	1740
GCTCAGATGT ACTGCTTGGT AAAAGATTGG CCTCCAATCA AGCCTGAACA GGCTATGGAG	1800

CTTCTGGACT	GCAATTACCC	AGATCCTATG	GTTTCGAGGTT	TTGCTGTTCG	GTGCTTAGAA	1860
AAATATTTAA	CAGATGACAA	ACTTTCTCAG	TACCTAATTC	AGCTAGTACA	GGTACTAAAA	1920
TATGAACAGT	ATTTGGATAA	CCTGCTTGTG	AGATTTTTAC	TCAAAAAAGC	GTAACTAAT	1980
CAAAGGATCG	GTCACTTTTT	CTTTTGGCAT	TTAAATCTG	AGATGCACAA	TAAACAGTT	2040
AGTCAGAGGT	TTGGCCTGCT	TTTGGAGTCC	TATTGCCGTG	CATGTGGGAT	GSTATCTGAAG	2100
CACCTTAATA	GGCAAGTTGA	GGCTATGGAA	AAGCTCATT	ACTTGACTGA	CATTCTCAAA	2160
CAAGAGAAGA	AGGATGAAAC	ACAAAAGGTA	CAGATGAAGT	TTTTAGTTGA	GCAAATGCGG	2220
CGACCAGATT	TCATGGATGC	TCTCCAGGGC	TTTCTGTCTC	CTCTAAACCC	TGCTCATCAG	2280
CTGGGAAATC	TCAGGCTTGA	AGAGTGTCTG	ATTATGTCTT	CTGCAAAAAG	GCCACTGTGG	2340
TTGAATTGGG	AGAACCCAGA	CATCATGTCA	GAATTACTCT	TTCAGAACAA	TGAGATCATC	2400
TTTAAAAATG	GGGATGATTT	ACGGCAAGAT	ATGCTAACCC	TTCAGATTAT	TCGCATTATG	2460
GAAAATATCT	GGCAAAATCA	AGGTCTTGAT	CTTCGAATGT	TACCTTATGG	ATGTCTGTCA	2520
ATCGGTGACT	GTGTGGGACT	TATCGAGGTG	GTGAGAAATT	CTCACACTAT	AATGCAGATT	2580
CAGTGTAAG	GAGGCCTGAA	AGGTGCACTG	CAGTTTAACA	GCCACACACT	CCATCAGTGG	2640
CTCAAAGACA	AGAACAAGGG	GGAAATATAT	GATGCGGCCA	TCGATTTGTT	TACACGATCA	2700
TGTGCTGGAT	ATTGTGTTGC	CACCTTCATT	TTGGGAATTG	GAGATCGTCA	CAATAGTAAT	2760
ATCATGGTTA	AAGATGATGG	ACAACGTGTT	CATATAGATT	TTGGACACTT	TTTGGATCAC	2820
AAGAAGAAAA	AATTTGGTTA	TAAACGAGAG	CGCGTGCCGT	TTGTTTTGAC	ACAAGATTTC	2880
TTAATAGTGA	TTAGTAAAGG	AGCCCAAGAA	TGCACAAAGA	CAAGAGAATT	TGAGAGGTTT	2940
CAGGAGATGT	GTTACAAGGC	TTATCTAGCT	ATTCGGCAGC	ATGCCAATCT	CTTCATAAAT	3000
CTTTTCTCAA	TGATGCTTGG	CTCTGGAATG	CCAGAACTGC	AATCTTTTGA	TGATATTGCA	3060
TACATTCGAA	AGACCCTAGC	TTTAGATAAA	ACTGAGCAAG	AGGCTTTGGA	GTATTCATG	3120
AAACAAATGA	ATGATGCACA	CCATGGTGGC	TGGACAACAA	AAATGGATTG	GATCTTCCAC	3180
ACAATTAAGC	AGCATGCTTT	GAACTGA				3207

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear



(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Met Pro Pro Arg Pro Ser Ser Gly Glu Leu Trp Gly Ile His Leu Met  
1 5 10 15

Pro Pro Arg Ile Leu Val Glu Cys Leu Leu Pro Asn Gly Met Ile Val  
20 25 30

Thr Leu Glu Cys Leu Arg Glu Ala Thr Leu Val Thr Ile Lys His Glu  
35 40 45

Leu Phe Lys Glu Ala Arg Lys Tyr Pro Leu His Gln Leu Leu Gln Asp  
50 55 60

Glu Ser Ser Tyr Ile Phe Val Ser Val Thr Gln Glu Ala Glu Arg Glu  
65 70 75 80

Glu Phe Phe Asp Glu Thr Arg Arg Leu Cys Asp Leu Arg Leu Phe Gln  
85 90 95

Pro Phe Leu Lys Val Ile Glu Pro Val Gly Asn Arg Glu Glu Lys Ile  
100 105 110

Leu Asn Arg Glu Ile Gly Phe Ala Ile Gly Met Pro Val Cys Glu Phe  
115 120 125

Asp Met Val Lys Asp Pro Glu Val Gln Asp Phe Arg Arg Asn Ile Leu  
130 135 140

Asn Val Cys Lys Glu Ala Val Asp Leu Arg Asp Leu Asn Ser Pro His  
145 150 155 160

Ser Arg Ala Met Tyr Val Tyr Pro Pro His Val Glu Ser Ser Pro Glu  
165 170 175

Leu Pro Lys His Ile Tyr Asn Lys Leu Asp Arg Gly Gln Ile Ile Val  
180 185 190

Val Ile Trp Val Ile Val Ser Pro Asn Asn Asp Lys Gln Lys Tyr Thr  
195 200 205

Leu Lys Ile Asn His Asp Cys Val Pro Glu Gln Val Ile Ala Glu Ala  
210 215 220

Ile Arg Lys Lys Thr Arg Ser Met Leu Leu Ser Ser Glu Gln Leu Lys  
225 230 235 240

Leu Cys Val Leu Glu Tyr Gln Gly Lys Tyr Ile Leu Lys Val Cys Gly  
245 250 255

Cys Asp Glu Tyr Phe Leu Glu Lys Tyr Pro Leu Ser Gln Tyr Lys Tyr  
260 265 270

Ile Arg Ser Cys Ile Met Leu Gly Arg Met Pro Asn Leu Lys Met Met  
275 280 285

Ala Lys Glu Ser Leu Tyr Ser Gln Leu Pro Met Asp Cys Phe Thr Met  
290 295 300

Pro Ser Tyr Ser Arg Arg Ile Ser Thr Ala Thr Pro Tyr Met Asn Gly  
305 310 315 320

Glu Thr Ser Thr Lys Ser Leu Trp Val Ile Asn Arg Ala Leu Arg Ile  
325 330 335

Lys Ile Leu Cys Ala Thr Tyr Val Asn Leu Asn Ile Arg Asp Ile Asp  
340 345 350

Lys Ile Tyr Val Arg Thr Gly Ile Tyr His Gly Gly Glu Pro Leu Cys  
355 360 365

Asp Asn Val Asn Thr Gln Arg Val Pro Cys Ser Asn Pro Arg Trp Asn  
370 375 380

Glu Trp Leu Asn Tyr Asp Ile Tyr Ile Pro Asp Leu Pro Arg Ala Ala  
385 390 395 400

Arg Leu Cys Leu Ser Ile Cys Ser Val Lys Gly Arg Lys Gly Ala Lys  
405 410 415

Glu Glu His Cys Pro Leu Ala Trp Gly Asn Ile Asn Leu Phe Asp Tyr  
420 425 430

Thr Asp Thr Leu Val Ser Gly Lys Met Ala Leu Asn Leu Trp Pro Val  
435 440 445

Pro His Gly Leu Glu Asp Leu Leu Asn Pro Ile Gly Val Thr Gly Ser  
450 455 460

Asn Pro Asn Lys Glu Thr Pro Cys Leu Glu Leu Glu Phe Asp Trp Phe  
465 470 475 480

Ser Ser Val Val Lys Phe Pro Asp Met Ser Val Ile Glu Glu His Ala  
485 490 495

Asn Trp Ser Val Ser Arg Glu Ala Gly Phe Ser Tyr Ser His Ala Gly  
500 505 510

Leu Ser Asn Arg Leu Ala Arg Asp Asn Glu Leu Arg Glu Asn Asp Lys  
515 520 525

Glu Gln Leu Lys Ala Ile Ser Thr Arg Asp Pro Leu Ser Glu Ile Thr  
530 535 540

Glu Gln Glu Lys Asp Phe Leu Trp Ser His Arg His Tyr Cys Val Thr  
545 550 555 560

Ile Pro Glu Ile Leu Pro Lys Leu Leu Leu Ser Val Lys Trp Asn Ser  
565 570 575

Arg Asp Glu Val Ala Gln Met Tyr Cys Leu Val Lys Asp Trp Pro Pro  
580 585 590

Ile Lys Pro Glu Gln Ala Met Glu Leu Leu Asp Cys Asn Tyr Pro Asp  
595 600 605

Pro Met Val Arg Gly Phe Ala Val Arg Cys Leu Glu Lys Tyr Leu Thr  
610 615 620

Asp Asp Lys Leu Ser Gln Tyr Leu Ile Gln Leu Val Gln Val Leu Lys  
625 630 635 640

Tyr Glu Gln Tyr Leu Asp Asn Leu Leu Val Arg Phe Leu Leu Lys Lys  
645 650 655

Ala Leu Thr Asn Gln Arg Ile Gly His Phe Phe Phe Trp His Leu Lys  
660 665 670

Ser Glu Met His Asn Lys Thr Val Ser Gln Arg Phe Gly Leu Leu Leu  
675 680 685

Glu Ser Tyr Cys Arg Ala Cys Gly Met Tyr Leu Lys His Leu Asn Arg  
690 695 700

Gln Val Glu Ala Met Glu Lys Leu Ile Asn Leu Thr Asp Ile Leu Lys  
705 710 715 720

Gln Glu Arg Lys Asp Glu Thr Gln Lys Val Gln Met Lys Phe Leu Val  
725 730 735

Glu Gln Met Arg Arg Pro Asp Phe Met Asp Ala Leu Gln Gly Leu Leu  
740 745 750

Ser Pro Leu Asn Pro Ala His Gln Leu Gly Asn Leu Arg Leu Lys Glu  
755 760 765

Cys Arg Ile Met Ser Ser Ala Lys Arg Pro Leu Trp Leu Asn Trp Glu  
770 775 780

Asn Pro Asp Ile Met Ser Glu Leu Leu Phe Gln Asn Asn Glu Ile Ile  
785 790 795 800

Phe Lys Asn Gly Asp Asp Leu Arg Gln Asp Met Leu Thr Leu Gln Ile  
805 810 815

Ile Arg Ile Met Glu Asn Ile Trp Gln Asn Gln Gly Leu Asp Leu Arg  
820 825 830

Met Leu Pro Tyr Gly Cys Leu Ser Ile Gly Asp Cys Val Gly Leu Ile  
835 840 845

Glu Val Val Arg Asn Ser His Thr Ile Met Gln Ile Gln Cys Lys Gly  
850 855 860

Gly Leu Lys Gly Ala Leu Gln Phe Asn Ser His Thr Leu His Gln Trp  
865 870 875 880

Leu Lys Asp Lys Asn Lys Gly Glu Ile Tyr Asp Ala Ala Ile Asp Leu  
885 890 895

Phe Thr Arg Ser Cys Ala Gly Tyr Cys Val Ala Thr Phe Ile Leu Gly  
900 905 910

Ile Gly Asp Arg His Asn Ser Asn Ile Met Val Lys Asp Asp Gly Gln  
915 920 925

Leu Phe His Ile Asp Phe Gly His Phe Leu Asp His Lys Lys Lys Lys  
 930 935 940

Phe Gly Tyr Lys Arg Glu Arg Val Pro Phe Val Leu Thr Gln Asp Phe  
 945 950 955 960

Leu Ile Val Ile Ser Lys Gly Ala Gln Glu Cys Thr Lys Thr Arg Glu  
 965 970 975

Phe Glu Arg Phe Gln Glu Met Cys Tyr Lys Ala Tyr Leu Ala Ile Arg  
 980 985 990

Gln His Ala Asn Leu Phe Ile Asn Leu Phe Ser Met Met Leu Gly Ser  
 995 1000 1005

Gly Met Pro Glu Leu Gln Ser Phe Asp Asp Ile Ala Tyr Ile Arg Lys  
 1010 1015 1020

Thr Leu Ala Leu Asp Lys Thr Glu Gln Glu Ala Leu Glu Tyr Phe Met  
 1025 1030 1035 1040

Lys Gln Met Asn Asp Ala His His Gly Gly Trp Thr Thr Lys Met Asp  
 1045 1050 1055

Trp Ile Phe His Thr Ile Lys Gln His Ala Leu Asn Xaa Lys Ile Thr  
 1060 1065 1070

Glu Lys Met Lys Ala His Ser Gly  
 1075 1080

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1069 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Met Pro Pro Arg Pro Ser Ser Gly Glu Leu Trp Gly Ile His Leu Met  
 1 5 10 15

Pro Pro Arg Ile Leu Val Glu Cys Leu Leu Pro Asn Gly Met Ile Val  
 20 25 30

Thr Leu Glu Cys Leu Arg Glu Ala Thr Leu Ile Thr Ile Lys His Glu  
35 40 45

Leu Phe Lys Glu Ala Arg Lys Tyr Pro Leu His Gln Leu Leu Gln Asp  
50 55 60

Glu Ser Ser Tyr Ile Phe Val Ser Val Thr Gln Glu Ala Glu Arg Glu  
65 70 75 80

Glu Phe Phe Asp Glu Thr Arg Arg Leu Cys Asp Leu Arg Leu Phe Gln  
85 90 95

Pro Phe Leu Lys Val Ile Glu Pro Val Gly Asn Arg Glu Glu Lys Ile  
100 105 110

Leu Asn Arg Glu Ile Gly Phe Ala Ile Gly Met Pro Val Cys Glu Phe  
115 120 125

Asp Met Val Lys Asp Pro Glu Val Gln Asp Phe Arg Arg Asn Ile Leu  
130 135 140

Asn Val Cys Lys Glu Ala Val Asp Leu Arg Asp Leu Asn Ser Pro His  
145 150 155 160

Ser Arg Ala Met Tyr Val Tyr Pro Pro Asn Val Glu Ser Ser Pro Glu  
165 170 175

Leu Pro Lys His Ile Tyr Asn Lys Leu Asp Lys Gly Gln Ile Ile Val  
180 185 190

Val Ile Trp Val Ile Val Ser Pro Asn Asn Asp Lys Gln Lys Tyr Thr  
195 200 205

Leu Lys Ile Asn His Asp Cys Val Pro Glu Gln Val Ile Ala Glu Ala  
210 215 220

Ile Arg Lys Lys Thr Arg Ser Met Leu Leu Ser Ser Glu Gln Leu Lys  
225 230 235 240

Leu Cys Val Leu Glu Tyr Gln Gly Lys Tyr Ile Leu Lys Val Cys Gly  
245 250 255

Cys Asp Glu Tyr Phe Leu Glu Lys Tyr Pro Leu Ser Gln Tyr Lys Tyr  
260 265 270

Ile Arg Ser Cys Ile Met Leu Gly Arg Met Pro Asn Leu Met Leu Met  
275 280 285

Ala Lys Glu Ser Leu Tyr Ser Gln Leu Pro Met Asp Cys Phe Thr Met  
290 295 300

Pro Ser Tyr Ser Arg Arg Ile Ser Thr Ala Thr Pro Tyr Met Asn Gly  
305 310 315 320

Glu Thr Ser Thr Lys Ser Leu Trp Val Ile Asn Ser Ala Leu Arg Ile  
325 330 335

Lys Ile Leu Cys Ala Thr Tyr Val Asn Val Asn Ile Arg Asp Ile Asp  
340 345 350

Lys Ile Tyr Val Arg Thr Gly Ile Tyr His Gly Gly Glu Pro Leu Cys  
355 360 365

Asp Asn Val Asn Thr Gln Arg Val Pro Cys Ser Asn Pro Arg Trp Asn  
370 375 380

Glu Trp Leu Asn Tyr Asp Ile Tyr Ile Pro Asp Leu Pro Arg Ala Ala  
385 390 395 400

Arg Leu Cys Leu Ser Ile Cys Ser Val Lys Gly Arg Lys Gly Ala Lys  
405 410 415

Glu Glu His Cys Pro Leu Ala Trp Gly Asn Ile Asn Leu Phe Asp Tyr  
420 425 430

Thr Asp Thr Leu Val Ser Gly Lys Met Ala Leu Asn Leu Trp Pro Val  
435 440 445

Pro His Gly Leu Glu Asp Leu Leu Asn Pro Ile Gly Val Thr Gly Ser  
450 455 460

Asn Pro Asn Lys Glu Thr Pro Cys Leu Glu Leu Glu Phe Asp Trp Phe  
465 470 475 480

Ser Ser Val Val Lys Phe Pro Asp Met Ser Val Ile Glu Glu His Ala  
485 490 495

Asn Trp Ser Val Ser Arg Glu Ala Gly Phe Ser Tyr Ser His Ala Gly  
500 505 510

Leu Ser Asn Arg Leu Ala Arg Asp Asn Glu Leu Arg Glu Asn Asp Lys  
515 520 525

Glu Gln Leu Arg Ala Ile Cys Thr Arg Asp Pro Leu Ser Glu Ile Thr  
530 535 540

Glu Gln Glu Lys Asp Phe Leu Trp Ser His Arg His Tyr Cys Val Thr  
545 550 555 560

Ile Pro Glu Ile Leu Pro Lys Leu Leu Leu Ser Val Lys Trp Asn Ser  
565 570 575

Arg Asp Glu Val Ala Gln Met Tyr Cys Leu Val Lys Asp Trp Pro Pro  
580 585 590

Ile Lys Pro Glu Gln Ala Met Glu Leu Leu Asp Cys Asn Tyr Pro Asp  
595 600 605

Pro Met Val Arg Gly Phe Ala Val Arg Cys Leu Glu Lys Tyr Leu Thr  
610 615 620

Asp Asp Lys Leu Ser Gln Tyr Leu Ile Gln Leu Val Gln Val Leu Lys  
625 630 635 640

Tyr Glu Gln Tyr Leu Asp Asn Leu Leu Val Arg Phe Leu Leu Lys Lys  
645 650 655

Ala Leu Thr Asn Gln Arg Ile Gly His Phe Phe Phe Trp His Leu Lys  
660 665 670

Ser Glu Met His Asn Lys Thr Val Ser Gln Arg Phe Gly Leu Leu Leu  
675 680 685

Glu Ser Tyr Cys Arg Ala Cys Gly Met Tyr Leu Lys His Leu Asn Arg  
690 695 700

Gln Val Glu Ala Met Glu Lys Leu Ile Asn Leu Thr Asp Ile Leu Lys  
705 710 715 720

Gln Glu Lys Lys Asp Glu Thr Gln Lys Val Gln Met Lys Phe Leu Val  
725 730 735



Glu Gln Met Arg Arg Pro Asp Phe Met Asp Ala Leu Gln Gly Phe Leu  
740 745 750

Ser Pro Leu Asn Pro Ala His Gln Leu Gly Asn Leu Arg Leu Glu Glu  
755 760 765

Cys Arg Ile Met Ser Ser Ala Lys Arg Pro Leu Trp Leu Asn Trp Glu  
770 775 780

Asn Pro Asp Ile Met Ser Glu Leu Leu Phe Gln Asn Asn Glu Ile Ile  
785 790 795 800

Phe Lys Asn Gly Asp Asp Leu Arg Gln Asp Met Leu Thr Leu Gln Ile  
805 810 815

Ile Arg Ile Met Glu Asn Ile Trp Gln Asn Gln Gly Leu Asp Leu Arg  
820 825 830

Met Leu Pro Tyr Gly Cys Leu Ser Ile Gly Asp Cys Val Gly Leu Ile  
835 840 845

Glu Val Val Arg Asn Ser His Thr Ile Met Gln Ile Gln Cys Lys Gly  
850 855 860

Gly Leu Lys Gly Ala Leu Gln Phe Asn Ser His Thr Leu His Gln Trp  
865 870 875 880

Leu Lys Asp Lys Asn Lys Gly Glu Ile Tyr Asp Ala Ala Ile Asp Leu  
885 890 895

Phe Thr Arg Ser Cys Ala Gly Tyr Cys Val Ala Thr Phe Ile Leu Gly  
900 905 910

Ile Gly Asp Arg His Asn Ser Asn Ile Met Val Lys Asp Asp Gly Gln  
915 920 925

Leu Phe His Ile Asp Phe Gly His Phe Leu Asp His Lys Lys Lys Lys  
930 935 940

Phe Gly Tyr Lys Arg Glu Arg Val Pro Phe Val Leu Thr Gln Asp Phe  
945 950 955 960

Leu Ile Val Ile Ser Lys Gly Ala Gln Glu Cys Thr Lys Thr Arg Glu  
965 970 975

Phe Glu Arg Phe Gln Glu Met Cys Tyr Lys Ala Tyr Leu Ala Ile Arg  
980 985 990

Gln His Ala Asn Leu Phe Ile Asn Leu Phe Ser Met Met Leu Gly Ser  
995 1000 1005

Gly Met Pro Glu Leu Gln Ser Phe Asp Asp Ile Ala Tyr Ile Arg Lys  
1010 1015 1020

Thr Leu Ala Leu Asp Lys Thr Glu Gln Glu Ala Leu Glu Tyr Phe Met  
1025 1030 1035 1040

Lys Gln Met Asn Asp Ala His His Gly Gly Trp Thr Thr Lys Met Asp  
1045 1050 1055

Trp Ile Phe His Thr Ile Lys Gln His Ala Leu Asn Xaa  
1060 1065

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

GGA GAC GAC TTG CGA CAG GAT CAA CTT ATT CTT CAA ATC ATT TCA CTC	48
Gly Asp Asp Leu Arg Gln Asp Gln Leu Ile Leu Gln Ile Ile Ser Leu	
1 5 10 15	
ATG GAC AAG CTG TTA CGG AAA GAA AAT CTG GAC TTG AAA TTG ACA CCT	96
Met Asp Lys Leu Leu Arg Lys Glu Asn Leu Asp Leu Lys Leu Thr Pro	
20 25 30	
TAT AAG GTG TTA GCC ACC AGT ACA AAA CAT GGC TTC ATG CAG TTT ATC	144
Tyr Lys Val Leu Ala Thr Ser Thr Lys His Gly Phe Met Gln Phe Ile	
35 40 45	
CAG TCA GTT CCT GTG GCT GAA GTT CTT GAT ACA GAG GGA AGC ATT CAG	192
Gln Ser Val Pro Val Ala Glu Val Leu Asp Thr Glu Gly Ser Ile Gln	
50 55 60	

AAC	TTT	TTT	AGA	AAA	TAT	GCA	CCA	AGT	GAG	AAT	GGG	CCA	AAT	GGG	ATT	240
Asn	Phe	Phe	Arg	Lys	Tyr	Ala	Pro	Ser	Glu	Asn	Gly	Pro	Asn	Gly	Ile	
65					70					75					80	

AGT	GCT	GAG	GTC	ATG	GAC	ACT	TAC	GTT	AAA	AGC	TGT	GCT	GGA	TAT	TGC	288
Ser	Ala	Glu	Val	Met	Asp	Thr	Tyr	Val	Lys	Ser	Cys	Ala	Gly	Tyr	Cys	
				85					90					95		

GTG	ATC	ACC	TAT	ATA	CTT	GGA	GTT	GGA	GAC	AGG	CAC	CTG	GAT	AAC	CTT	336
Val	Ile	Thr	Tyr	Ile	Leu	Gly	Val	Gly	Asp	Arg	His	Leu	Asp	Asn	Leu	
			100					105					110			

TTG	CTA	ACC	AAA	ACA	GGC	AAA	CTC	TTC	CAC	ATC	GAT	TTC	GGC	CAC		381
Leu	Leu	Thr	Lys	Thr	Gly	Lys	Leu	Phe	His	Ile	Asp	Phe	Gly	His		
			115				120					125				

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Gly	Asp	Asp	Leu	Arg	Gln	Asp	Gln	Leu	Ile	Leu	Gln	Ile	Ile	Ser	Leu
1				5					10					15	

Met	Asp	Lys	Leu	Leu	Arg	Lys	Glu	Asn	Leu	Asp	Leu	Lys	Leu	Thr	Pro
			20					25					30		

Tyr	Lys	Val	Leu	Ala	Thr	Ser	Thr	Lys	His	Gly	Phe	Met	Gln	Phe	Ile
		35					40					45			

Gln	Ser	Val	Pro	Val	Ala	Glu	Val	Leu	Asp	Thr	Glu	Gly	Ser	Ile	Gln
	50					55					60				

Asn	Phe	Phe	Arg	Lys	Tyr	Ala	Pro	Ser	Glu	Asn	Gly	Pro	Asn	Gly	Ile
65					70					75					80

Ser	Ala	Glu	Val	Met	Asp	Thr	Tyr	Val	Lys	Ser	Cys	Ala	Gly	Tyr	Cys
				85					90					95	

Val Ile Thr Tyr Ile Leu Gly Val Gly Asp Arg His Leu Asp Asn Leu  
100 105 110

Leu Leu Thr Lys Thr Gly Lys Leu Phe His Ile Asp Phe Gly His  
115 120 125

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..393

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

GGG GAT GAC TTA CGG CAG GAC ATG CTA ACG CTG CAG ATG ATT CGC ATC	48
Gly Asp Asp Leu Arg Gln Asp Met Leu Thr Leu Gln Met Ile Arg Ile	
1 5 10 15	
ATG AGC AAG ATC TGG GTC CAG GAG GGG CTG GAC ATG CGC ATG GTC ATC	96
Met Ser Lys Ile Trp Val Gln Glu Gly Leu Asp Met Arg Met Val Ile	
20 25 30	
TTC CGC TGC TTC TCC ACC GGC CGG GGC AGA GGG ATG GTG GAG ATG ATC	144
Phe Arg Cys Phe Ser Thr Gly Arg Gly Arg Gly Met Val Glu Met Ile	
35 40 45	
CCT AAT GCT GAG ACC CTG CGT AAG ATC CAG GTG GAG CAT GGG GTG ACC	192
Pro Asn Ala Glu Thr Leu Arg Lys Ile Gln Val Glu His Gly Val Thr	
50 55 60	
GGC TCG TTC AAG GAC CGG CCC CTG GCA GAC CGG CTG CAG AAA CAC AAC	240
Gly Ser Phe Lys Asp Arg Pro Leu Ala Asp Arg Leu Gln Lys His Asn	
65 70 75 80	
CCT GGG GAG GAC GAG TAT GAG AAG GCT GTG GAG AAC TTT ATC TAC TCC	288
Pro Gly Glu Asp Glu Tyr Glu Lys Ala Val Glu Asn Phe Ile Tyr Ser	
85 90 95	
TGC GCT GGC TGC TGC GTG GCC ACG TAC GTC TTG GGC ATC TGT GAC CGA	336
Cys Ala Gly Cys Cys Val Ala Thr Tyr Val Leu Gly Ile Cys Asp Arg	
100 105 110	

CAT	AAT	GAC	AAC	ATC	ATG	CTG	AAG	ACC	ACT	GGT	CAC	ATG	TTC	CAC	ATC
His	Asn	Asp	Asn	Ile	Met	Leu	Lys	Thr	Thr	Gly	His	Met	Phe	His	Ile
		115					120					125			

GAC TTC GGC  
Asp Phe Gly  
130

(2) INFORMATION FOR SEQ ID NO: 41:

(ii) MOLECULE TYPE: protein

Gly Asp Asp Leu Arg Gln Asp Met Leu Thr Leu Gln Met Ile Arg Ile  
1 5 10 15

Phe Arg Cys Phe Ser Thr Gly Arg Gly Arg Gly Met Val Glu Met Ile  
35 40 45

Gly Ser Phe Lys Asp Arg Pro Leu Ala Asp Arg Leu Gln Lys His Asn  
65 70 75 80

Cys Ala Gly Cys Cys Val Ala Thr Tyr Val Leu Gly Ile Cys Asp Arg  
100 105 110

Asp Phe Gly  
130

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 66 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

Gly Asp Asp Leu Arg Gln Asp Gln Leu Val Val Gln Ile Ile Ser Leu  
1 5 10 15  
Met Asn Glu Leu Leu Lys Asn Glu Asn Val Asp Leu Lys Leu Thr Pro  
20 25 30  
Tyr Lys Ile Leu Ala Thr Gly Pro Gln Glu Gly Ala Ile Glu Phe Ile  
35 40 45  
Pro Asn Asp Thr Leu Ala Ser Ile Leu Ser Lys Tyr His Gly Ile Leu  
50 55 60  
Gly Tyr  
65

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 60 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

Leu Lys Leu His Tyr Pro Asp Glu Asn Ala Thr Leu Gly Val Gln Gly  
1 5 10 15  
Trp Val Leu Asp Asn Phe Val Lys Ser Cys Ala Gly Tyr Cys Val Ile  
20 25 30  
Thr Tyr Ile Leu Gly Val Gly Asp Arg His Leu Asp Asn Leu Leu Val  
35 40 45  
Thr Pro Asp Gly His Phe Phe His Ala Asp Phe Gly  
50 55 60

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Gly Asp Asp Leu Arg Gln Asp Gln Leu Ile Leu Gln Ile Ile Ser Leu  
1 5 10 15

Met Asp Lys Leu Leu Arg Lys Glu Asn Leu Asp Leu Lys Leu Thr Pro  
20 25 30

Tyr Lys Val Leu Ala Thr Ser Thr Lys His Gly Phe Met Gln Phe Ile  
35 40 45

Gln Ser Val Pro Val Ala Glu Val Leu Asp Thr Glu Gly Ser Ile Gln  
50 55 60

Asn Phe  
65

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Phe Arg Lys Tyr Ala Pro Ser Glu Asn Gly Pro Asn Gly Ile Ser Ala  
1 5 10 15

Glu Val Met Asp Thr Tyr Val Lys Ser Cys Ala Gly Tyr Cys Val Ile  
20 25 30

Thr Tyr Ile Leu Gly Val Gly Asp Arg His Leu Asp Asn Leu Leu Leu  
35 40 45

Thr Lys Thr Gly Lys Leu Phe His Ile Asp Phe Gly  
50 55 60

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Gly Asp Asp Leu Arg Gln Asp Met Leu Thr Leu Gln Ile Ile Arg Ile  
1 5 10 15

Met Glu Asn Ile Trp Gln Asn Gln Gly Leu Asp Leu Arg Met Leu Pro  
20 25 30

Tyr Gly Cys Leu Ser Ile Gly Asp Cys Val Gly Leu Ile Glu Val Val  
35 40 45

Arg Asn Ser His Thr Ile Met Gln Ile Gln Cys Lys Gly Gly Leu Lys  
50 55 60

Gly Ala Leu Gln Phe Asn Ser His Thr Leu His Gln Trp Leu Lys Asp  
65 70 75 80

Lys Asn Lys Gly Glu  
85

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 47 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

Ile Tyr Asp Ala Ala Ile Asp Leu Phe Thr Arg Ser Cys Ala Gly Tyr  
1 5 10 15

Cys Val Ala Thr Phe Ile Leu Gly Ile Gly Asp Arg His Asn Ser Asn  
20 25 30

Ile Met Val Lys Asp Asp Gly Gln Leu Phe His Ile Asp Phe Gly  
35 40 45



(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Gly Asp Asp Leu Arg Gln Asp Met Leu Thr Leu Gln Met Ile Arg Ile  
1 5 10 15

Met Ser Lys Ile Trp Val Gln Glu Gly Leu Asp Met Arg Met Val Ile  
20 25 30

Phe Arg Cys Phe Ser Thr Gly Arg Gly Arg Gly Met Val Glu Met Ile  
35 40 45

Pro Asn Ala Glu Thr Leu Arg Lys Ile Gln Val Glu His Gly Val Thr  
50 55 60

Gly Ser  
65

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

Phe Lys Asp Arg Pro Leu Ala Asp Arg Leu Gln Lys His Asn Pro Gly  
1 5 10 15

Glu Asp Glu Tyr Glu Lys Ala Val Glu Asn Phe Ile Tyr Ser Cys Ala  
20 25 30

Gly Cys Cys Val Ala Thr Tyr Val Leu Gly Ile Cys Asp Arg His Asn  
35 40 45

Asp Asn Ile Met Leu Lys Thr Thr Gly His Met Phe His Ile Asp Phe  
50 55 60

Gly  
65

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Gly Asp Asp Leu Arg Gln Asp Leu Leu Gln Ile Ile Met Glu Leu Asp  
1 5 10 15

Leu Pro Tyr Leu Thr Gly Gly Ile Glu Ile Asn Gly Ile Gly Leu Asn  
20 25 30

Ile Asp Phe Val Ser Cys Ala Gly Tyr Cys Val Thr Tyr Ile Leu Gly  
35 40 45

Gly Asp Arg His Asp Asn Gly Leu Phe His Ile Asp Phe Gly  
50 55 60